
MAAEAQPLGLSKPGPTWPELLGSNAWAGLLNPLNDE
LRELLLRCGDFCQVTYDTFINDQNSSYCGGSSRYGKA
DLLHKTAFPGGADRFDVVAYLYATAKVSVPEAFLLK
SRSREKWDRESNWIGYVVVSNDETSRVAGRREVYVV
WRGTCRDYEWVDVLGAQLESAHPLLRTQQTTHVEKV
ENEEKKSIHKSSWYDCFNINLLGSASKDKGKGSDDD
DDDDPKVMQGWMTIYTSEDPKSPFTKLSARTQLQTK
LKQLMTKYKDETLSITFAGHSLGATLSVVSAFDIVE
NLTTEIPVTAVVFGCPKVGNKKFQQLFDSYPNLNVL
HVRNVIDLIPLYPVKLMGYVNIGIELEIDSSRKSTFL
KDSKNPSDWHNLQAILHVVSGWHGVKGEFKVVNKRS
VALVNKSCDFLKEECLVPPAWWVVQNKGMVLNKDGE
WVLAPPEEDPTPEFD

FIG.1

```
          1                                                  50
carlip ......MAAE AQPLGLSKPG PTWPELLGSN AWAGLLNPLN DELRELLLRC
arlipl MKRKKKEEEE EKLIVTREFA KRWRDLSGQN HWKGMLQPLD QDLREYIIHY
ipolip .......... .....MSGIA KRWKVLSGSD NWEGLLEPLD SDLRRYLIHY
arlipi MTAEDIRRRD KKTEEERRLR DTWRKIQGED DWAGLMDPMD PILRSELIRY

          51                                                 100
carlip GDFCQVTYDT FINDQNSSYC GSSRYGKADL LHKTAFPGGA D..RFDVVAY
arlipl GEMAQAGYDT FNINTESQFA GASIYSRKDF FAKVGLEIAH PYTKYKVTKF
ipolip GTMVSPATDS FINEAASKNV GLPRYARRNL LANCGLVKGN PF.KYEVTKY
arlipi GEMACACYDA FDFDPASKYC GTSRFTRLEF FDSLGMIDSG ....YEVARY

          101                                                150
carlip LYATAKVSVP .EAFLLKSRS REKWDRESNW IGYVVVSNDE TSRVA.GRRE
arlipl IYATSDIHVP .ESFLLFPIS REGWSKESNW MGYVAVTDDQ .GTALLGRRD
ipolip FYAPSTIPLP DEGYNVRATR ADAVLKESNW NGYVAVATDE .GKVALGRRD
arlipi LYATSNINLP ..NFFSKSRW SKVWSKNANW MGYVAVSDDE TSRNRLGRRD

          151                                                200
carlip VYVVWRGTCR DYEWVDVLGA QLESAHPLLR TQQTTHVEKV ENEEKKSIHK
arlipl IVVSWRGSVQ PLEWVEDFEF GLVNAI.... .......... ..........
ipolip ILIVWRGTIR KSEWNENLTF WFVKAP.... .......... ..........
arlipi IAIAWRGTVT KLEWIADLKD YLKPVT.... .......... ..........

          201                                                250
carlip SSWYDCFNIN LLGSASKDKG KGSDDDDDDD PKVMQGWMTI YTSEDPKSPF
arlipl .......... .......... KIFGERNDQ. VQIHQGWYSI YMSQDERSPF
ipolip .......... .......... LFFGQNSDP. L.VHKGWYDM YTTINQDSQL
arlipi .......... .......... ENKIRCPDPA VKVESGFLDL YTDKDTTCKF

          251                                                300
carlip TKLSARTQLQ TKLKQLMTKY KDET...LSI TFAGHSLGAT LSVVSAFDIV
arlipl TKTNARDQVL REVGRLLEKY KDEE...VSI TICGHSLGAA LATLSAIDIV
ipolip NEKSARDQIR EEVARLVELY KDED...ISI TVTGHSLGSS MATLNAVDLA
arlipi ARFSAREQIL TEVKRLVEEH GDDDDSDLSI TVTGHSLGGA LAILSAYDIA
```

FIG.2A

```
       301                                                        350
carlip ENLTTE.... ....IPVTAV VFGCPKVGNK KFQQLFDSYP NLNVLHVRNV
arlipl ANGYNRPKSR PDKSCPVTAF VFASPRVGDS DFRKLFSGLE DIRVLRTRNL
ipolip ANPINN.... .NKNILVTAF LYASPKVGDE NFKNVISNQQ NLRALRISDV
arlipi EMRLNR..SK KGKVIPVTVL TYGGPRVGNV RFRERMEEL. GVKVMRVVNV

       351                                                        400
carlip IDLIPLYPVK LMG..... ..... YVNIGIELEI DSRKSTFLKD
arlipl PDVIPIYPPI G..... ..... YSEVGDEFPI DTRKSPYMKS
ipolip NDIVTAVPPF GWKEGDNTAI L..... YGDVGVGLVI DSKKSHYLKP
arlipi HDVVPKSPGL FLNESRPHAL MKIAEGLPWC YSHVGEELAL DHQNSPFLKP

       401                                                        450
carlip SKNPSDWHNL QAILHVVSGW HGV.KGE.FK VVNKRSVALV NKSCDFLKEE
arlipl PGNLATFHCL EGYLHGVAGT QGTNKADLFR LDVERAIGLV NKSVDGLKDE
ipolip DFPNLSTHDL MLYMHAIDGY QGSQGG..FE RQEDFDLAKV NKYGDYLKAE
arlipi SVDVSTAHNL EAMLHLLDGY HG..KGERFV LSSGRDHALV NKASDFLKEH

       451                                                        500
carlip CLVPPAWWVV QNKGMVLNKD GEWVLAPP.. .EEDPTPEFD ..........
arlipl CMVPGKWRVL KNKGMAQQDD GSWELVDH.E IDDNEDLDF. ..........
ipolip YPIPIGWFNI KDKGMVQQDD GNYILDDH.E VDKTF..... ..........
arlipi LQIPPFWRQD ANKGMVRNSE GRWIQAERLR FEDHHSPDIH HHLSQLRLDH

       501
carlip ..
arlipl ..
ipolip
arlipi PC
```

FIG.2B

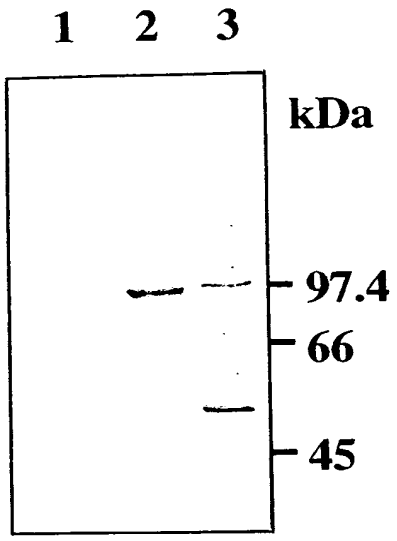


FIG.3

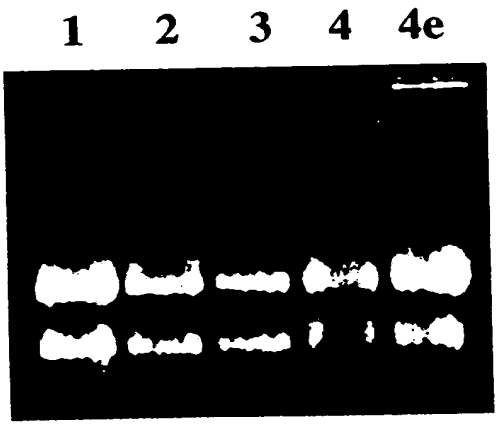


FIG.4A

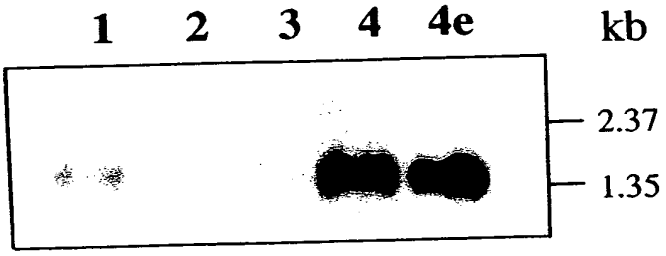


FIG.4B

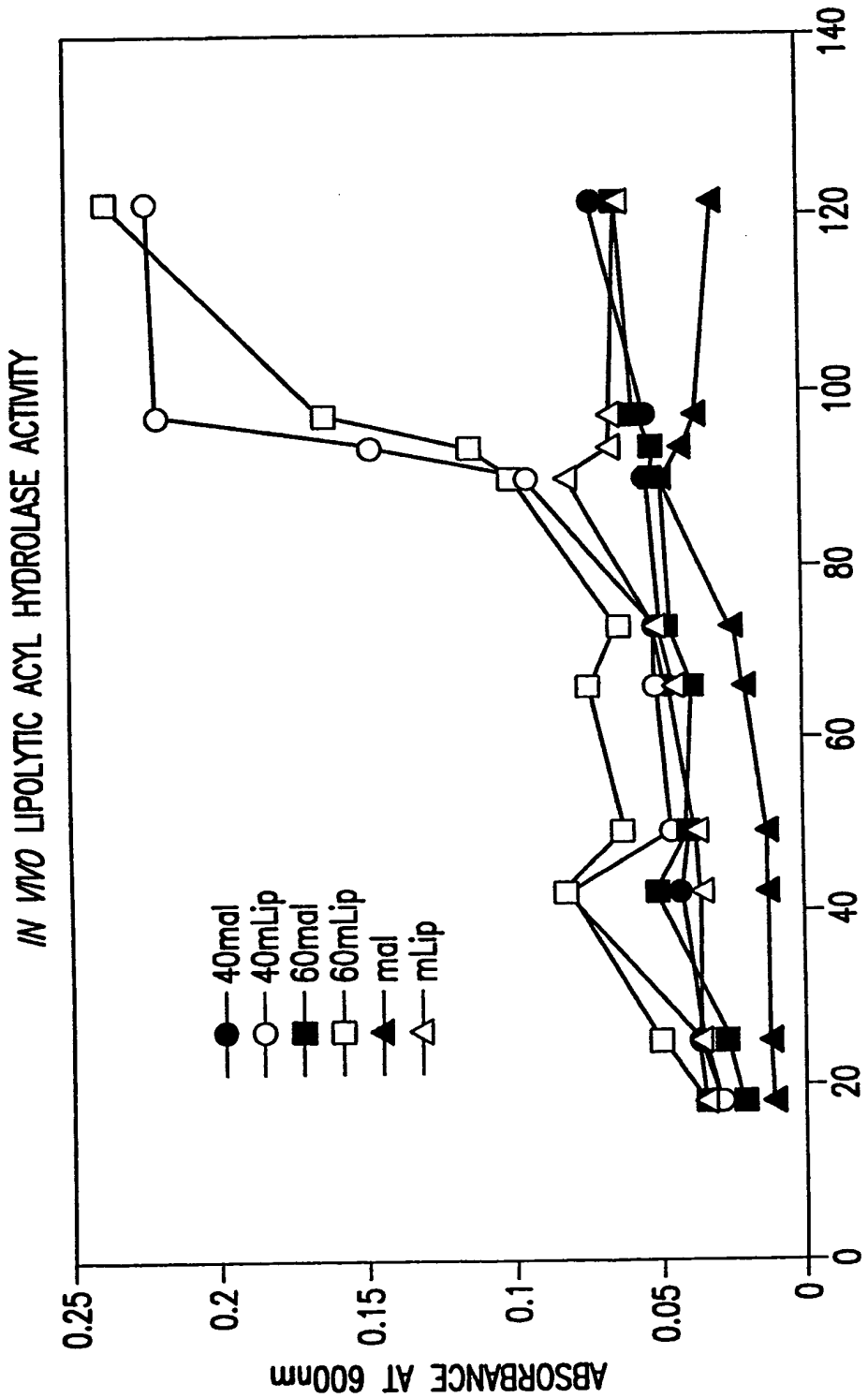

IN VIVO LIPOLYTIC ACYL HYDROLASE ACTIVITY
ABSORBANCE AT 600nm
0.25
0.2
0.15
0.1
0.05
0
0
20
40
60
80
100
120
140
TIME (hr)
40mal
40mLip
60mal
60mLip
mal
mLip

FIG.5

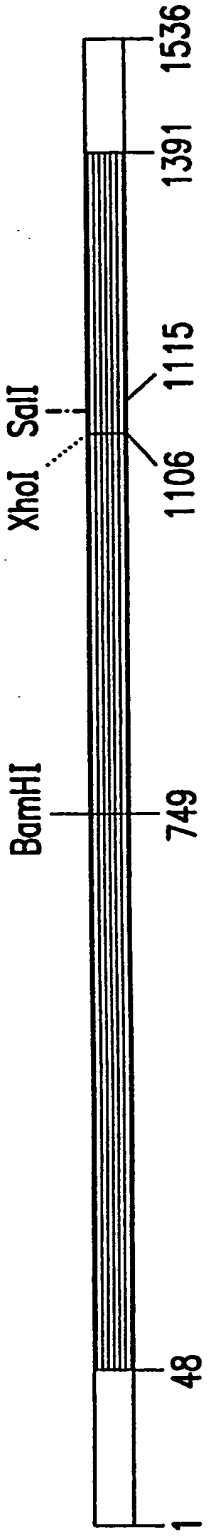


FIG. 6A

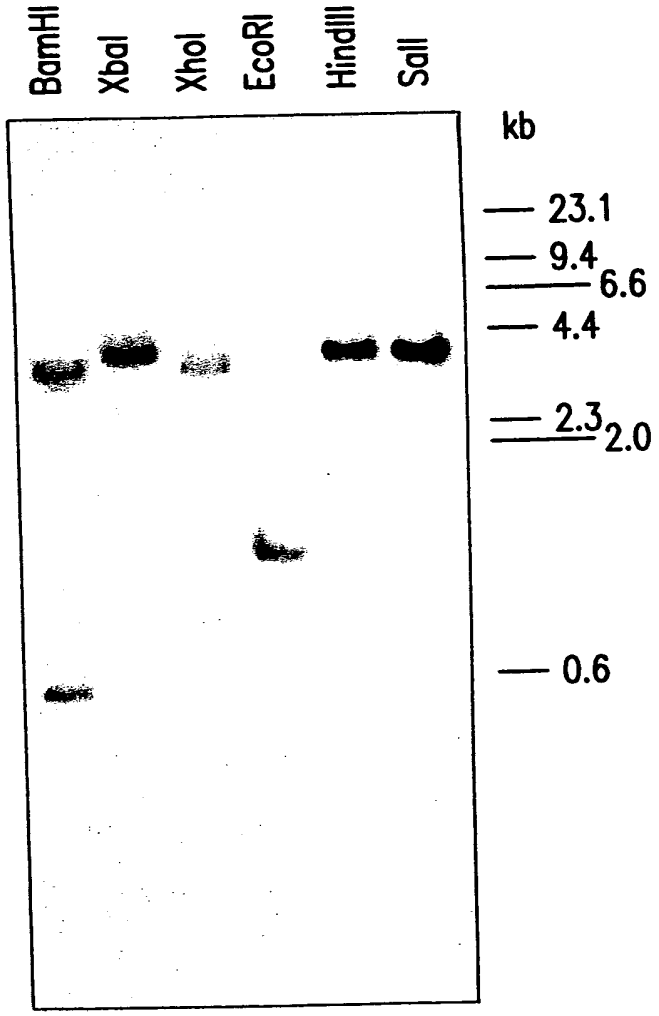


FIG.6B

GCACGAGCCATTCCAAAACTCCTTACACCACTCAAAACTATTCCAACATGGCTGCAGAAGCCCAACCTTTAGGCCTCTC
AAAGCCCGGCCCAACATGGCCCGAACTCCTCGGGTCCAACGCTTGGGCCGGGCTACTAAACCCGCTCAACGATGAGCTC
CGTGAGCTCCTCCTACGCTGCGGGGACTTCTGCCAGGTGACATACGACACCTTCATAAACGACCAGAACTCGTCCTACT
GCGGCAGCAGCCGCTACGGGAAGGCGGACCTACTTCATAAGACCGCCTTCCCGGGGGGCGCAGACCGGTTTGACGTGGT
GGCGTACTTGTACGCCACTGCGAAGGTCAGCGTCCCAgAGGCGTTTCTGCTGAAGTCGAGGTCGAGGGAGAAGTGGGAT
AGGGAATCGAATTGGATTGGGTATGTCGTGGTGTCGAATGACGAGACGAGTCGGGTGGCGGGACGAAgGGAGGTGTATG
TGGTGTGGAGAGGGACTTGTAgGGATTATGAGTGGGTTGATGTTCTTGGTGCTCAACTTGAGTCTGCTCATCCTTTGTT
ACGCACTCAACAAACTACTCATGTTGAAAAGGTGGAAAATGAGGAAAAGAAGAGCATTCATAAATCAAGTTGGTACGAC
TGTTTCAATATCAACCTACTAgGTTCCGCGTCCAAAGACAAAGGAAAAGGAAgCGACGACGACGATGATGACGACCCCA
AAGTGATGCAAGGTTGGATGACAATATACACATCGGAGGATCCCAAATCACCCTTCACAAAACTAAGTGCAAGAACACA
ACTTCAGACCAAACTCAAACAACTAATGACAAAATACAAAGACGAAACCCTAAGCATAACATTCGCCGGTCACAGCCTA
GGCGCGACACTATCAGTCGTGAGCGCCTTCGACATAGTGGAGAATCTCACGACCGAGATCCCAGTCACGGCCGTGGTCT
TCGGGTGCCCAAAAGTAGGCAACAAAAAATTCCAACAACTCTTCGACTCGTACCCAAACCTAAATGTCCTCCATGTAAG
GAATGTCATCGACCTGATCCCTCTGTATCCCGTGAAACTCATGGGTTACGTGAACATAGGAATCGAGCTGGAGATCGAC
TCGAGGAAGTCGACCTTTCTAAAGGACTCGAAAAACCCGAGTGATTGGCATAATTTGCAAGCAATATTGCATGTTGTAA
GTGGTTGGCATGGGGTTAAGGGGGAGTTTAAGGTTGTAAATAAGAGAAGTGTTGCATTGGTTAATAAGTCATGTGATTT
TCTTAAGGAAGAATGTTTGGTTCCTCCAGCTTGGTGGGTTGTGCAGAACAAAGGGATGGTTTTGAATAAGGATGGTGAG
TGGGTTTTGGCTCCTCCTGAGGAAGATCCTACTCCTGAATTTGATTGATAATATTTCATCATGTTTTATATTTTTATAA
ATTTTACTAAATTTACATGACAATTTATGGGACTAAGTTACTTATTTATATGTTTATTATATTTGAAATGTGTTTTAAG
TTACATAAAATTGCAATTAGTTTTAAAAAAAAAAAA

——————uncoding region of cDNA clone

FIG.7

```
Met Ala Ala Glu Ala Gln Pro Leu Gly Leu Ser Lys Pro Gly Pro Thr Trp Pro Glu Leu
 1               5                  10                  15                  20

Leu Gly Ser Asn Ala Trp Ala Gly Leu Leu Asn Pro Leu Asn Asp Glu Leu Arg Glu Leu
            21                  25                  30                  35      40

Leu Leu Arg Cys Gly Asp Phe Cys Gln Val Thr Tyr Asp Thr Phe Ile Asn Asp Gln Asn
            41                  45                  50                  55      60

Ser Ser Tyr Cys Gly Ser Ser Arg Tyr Gly Lys Ala Asp Leu Leu His Lys Thr Ala Phe
            61                  65                  70                  75      80

Pro Gly Gly Ala Asp Arg Phe Asp Val Val Ala Tyr Leu Tyr Ala Thr Ala Lys Val Ser
            81                  85                  90                  95     100

Val Pro Glu Ala Phe Leu Leu Lys Ser Arg Ser Arg Glu Lys Trp Asp Arg Glu Ser Asn
           101                 105                 110                 115     120

Trp Ile Gly Tyr Val Val Val Ser Asn Asp Glu Thr Ser Arg Val Ala Gly Arg Arg Glu
           121                 125                 130                 135     140

Val Tyr Val Val Trp Arg Gly Thr Cys Arg Asp Tyr Glu Trp Val Asp Val Leu Gly Ala
           141                 145                 150                 155     160

Gln Leu Glu Ser Ala His Pro Leu Leu Arg Thr Gln Gln Thr Thr His Val Glu Lys Val
           161                 165                 170                 175     180

Glu Asn Glu Glu Lys Lys Ser Ile His Lys Ser Ser Trp Tyr Asp Cys Phe Asn Ile Asn
           181                 185                 190                 195     200

Leu Leu Gly Ser Ala Ser Lys Asp Lys Gly Lys Gly Ser Asp Asp Asp Asp Asp Asp Asp
           201                 205                 210                 215     220
```

FIG.8A

Pro Lys Val Met Gln Gly Trp Met Thr Ile Tyr Thr Ser Glu Asp Pro Lys Ser Pro Phe
221 225 230 235 240

Thr Lys Leu Ser Ala Arg Thr Gln Leu Gln Thr Lys Leu Lys Gln Leu Met Thr Lys Tyr
241 245 250 255 260

Lys Asp Glu Thr Leu Ser Ile Thr Phe Ala Gly His Ser Leu Gly Ala Thr Leu Ser Val
261 265 270 275 280

Val Ser Ala Phe Asp Ile Val Glu Asn Leu Thr Thr Glu Ile Pro Val Thr Ala Val Val
281 285 290 295 300

Phe Gly Cys Pro Lys Val Gly Asn Lys Lys Phe Gln Gln Leu Phe Asp Ser Tyr Pro Asn
301 305 310 315 320

Leu Asn Val Leu His Val Arg Asn Val Ile Asp Leu Ile Pro Leu Tyr Pro Val Lys Leu
321 325 330 335 340

Met Gly Tyr Val Asn Ile Gly Ile Glu Leu Glu Ile Asp Ser Arg Lys Ser Thr Phe Leu
341 345 350 355 360

Lys Asp Ser Lys Asn Pro Ser Asp Trp His Asn Leu Gln Ala Ile Leu His Val Val Ser
361 365 370 375 380

Gly Trp His Gly Val Lys Gly Glu Phe Lys Val Val Asn Lys Arg Ser Val Ala Leu Val
381 385 390 395 400

Asn Lys Ser Cys Asp Phe Leu Lys Glu Glu Cys Leu Val Pro Pro Ala Trp Trp Val Val
401 405 410 415 420

Gln Asn Lys Gly Met Val Leu Asn Lys Asp Gly Glu Trp Val Leu Ala Pro Pro Glu Glu
421 425 430 435 440

Asp Pro Thr Pro Glu Phe Asp
441 445

FIG.8B

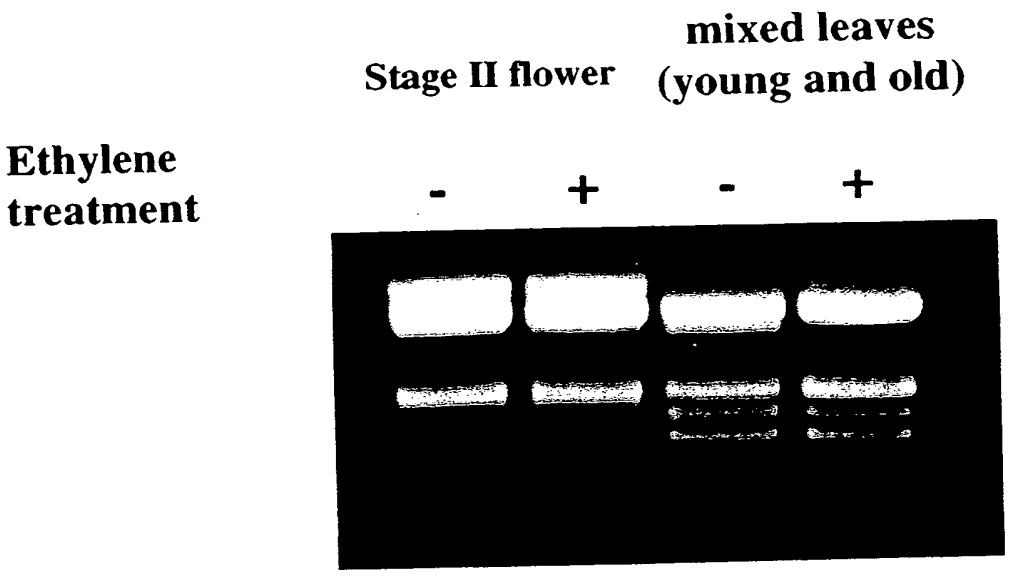


FIG.9A

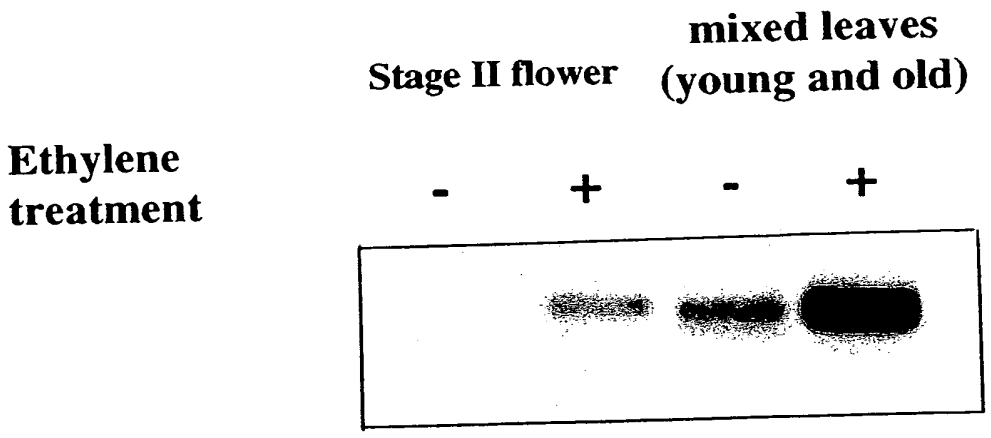


FIG.9B

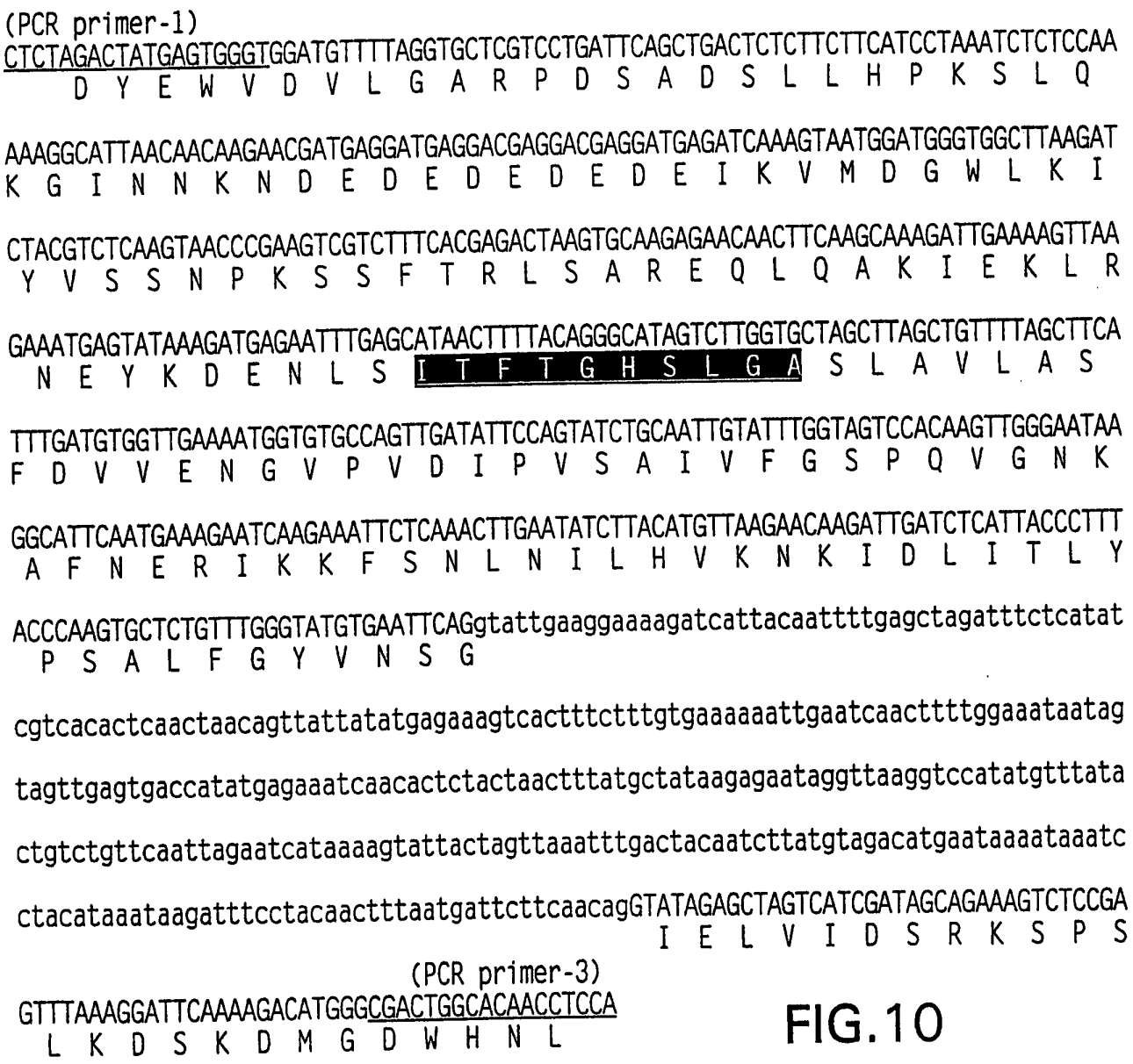

(PCR primer-1)
CTCTAGACTATGAGTGGGTGGATGTTTTAGGTGCTCGTCCTGATTCAGCTGACTCTCTTCTTCATCCTAAATCTCTCCAA
D Y E W V D V L G A R P D S A D S L L H P K S L Q
AAAGGCATTAACAACAAGAACGATGAGGATGAGGACGAGGACGAGGATGAGATCAAAGTAATGGATGGGTGGCTTAAGAT
K G I N N K N D E D E D E D E D E I K V M D G W L K I
CTACGTCTCAAGTAACCCGAAGTCGTCTTTCACGAGACTAAGTGCAAGAGAACAACTTCAAGCAAAGATTGAAAAGTTAA
Y V S S N P K S S F T R L S A R E Q L Q A K I E K L R
GAAATGAGTATAAAGATGAGAATTTGAGCATAACTTTTACAGGGCATAGTCTTGGTGCTAGCTTAGCTGTTTTAGCTTCA
N E Y K D E N L S I T F T G H S L G A S L A V L A S
TTTGATGTGGTTGAAAATGGTGTGCCAGTTGATATTCCAGTATCTGCAATTGTATTTGGTAGTCCACAAGTTGGGAATAA
F D V V E N G V P V D I P V S A I V F G S P Q V G N K
GGCATTCAATGAAAGAATCAAGAAATTCTCAAACTTGAATATCTTACATGTTAAGAACAAGATTGATCTCATTACCCTTT
A F N E R I K K F S N L N I L H V K N K I D L I T L Y
ACCCAAGTGCTCTGTTTGGGTATGTGAATTCAGgtattgaaggaaaagatcattacaattttgagctagatttctcatat
P S A L F G Y V N S G
cgtcacactcaactaacagttattatatgagaaagtcactttctttgtgaaaaaattgaatcaacttttggaaataatag
tagttgagtgaccatatgagaaatcaacactctactaactttatgctataagagaataggttaaggtccatatgtttata
ctgtctgttcaattagaatcataaaagtattactagttaaatttgactacaatcttatgtagacatgaataaaataaatc
ctacataaataagatttcctacaactttaatgattcttcaacagGTATAGAGCTAGTCATCGATAGCAGAAAGTCTCCGA
I E L V I D S R K S P S
(PCR primer-3)
GTTTAAAGGATTCAAAAGACATGGGCGACTGGCACAACCTCCA
L K D S K D M G D W H N L

FIG.10

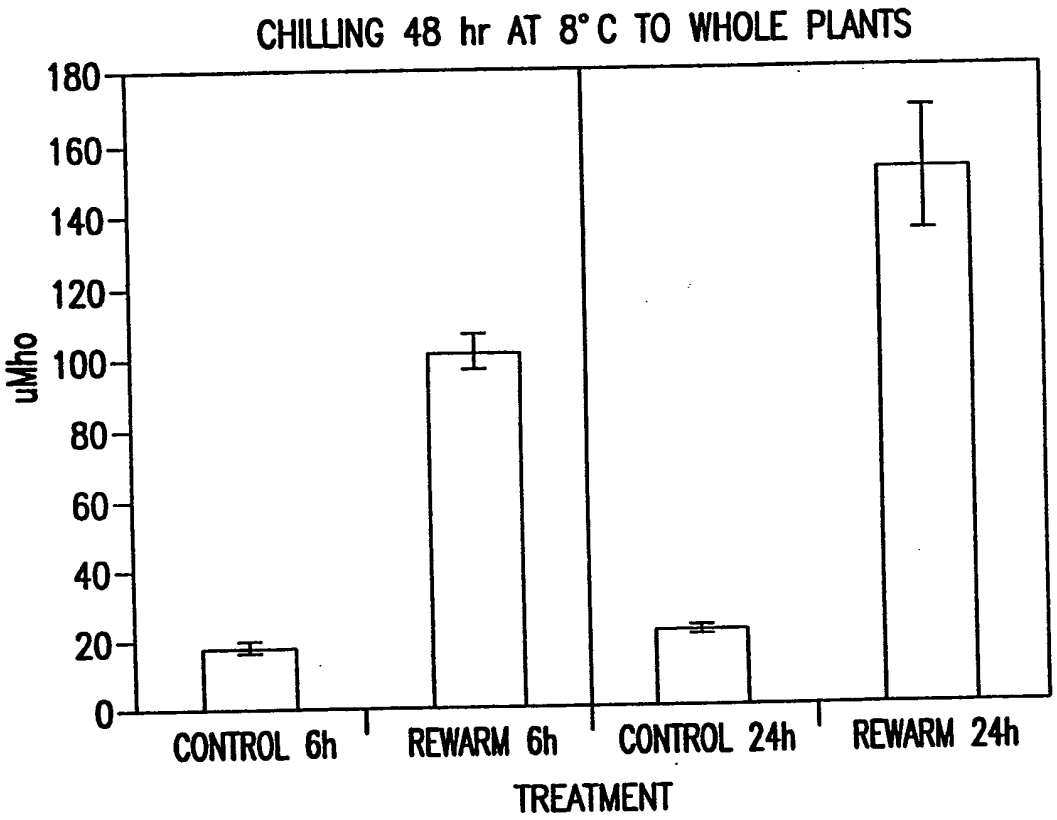

CHILLING 48 hr AT 8° C TO WHOLE PLANTS
uMho
180
160
140
120
100
80
60
40
20
0
CONTROL 6h
REWARM 6h
CONTROL 24h
REWARM 24h
TREATMENT

FIG. 11

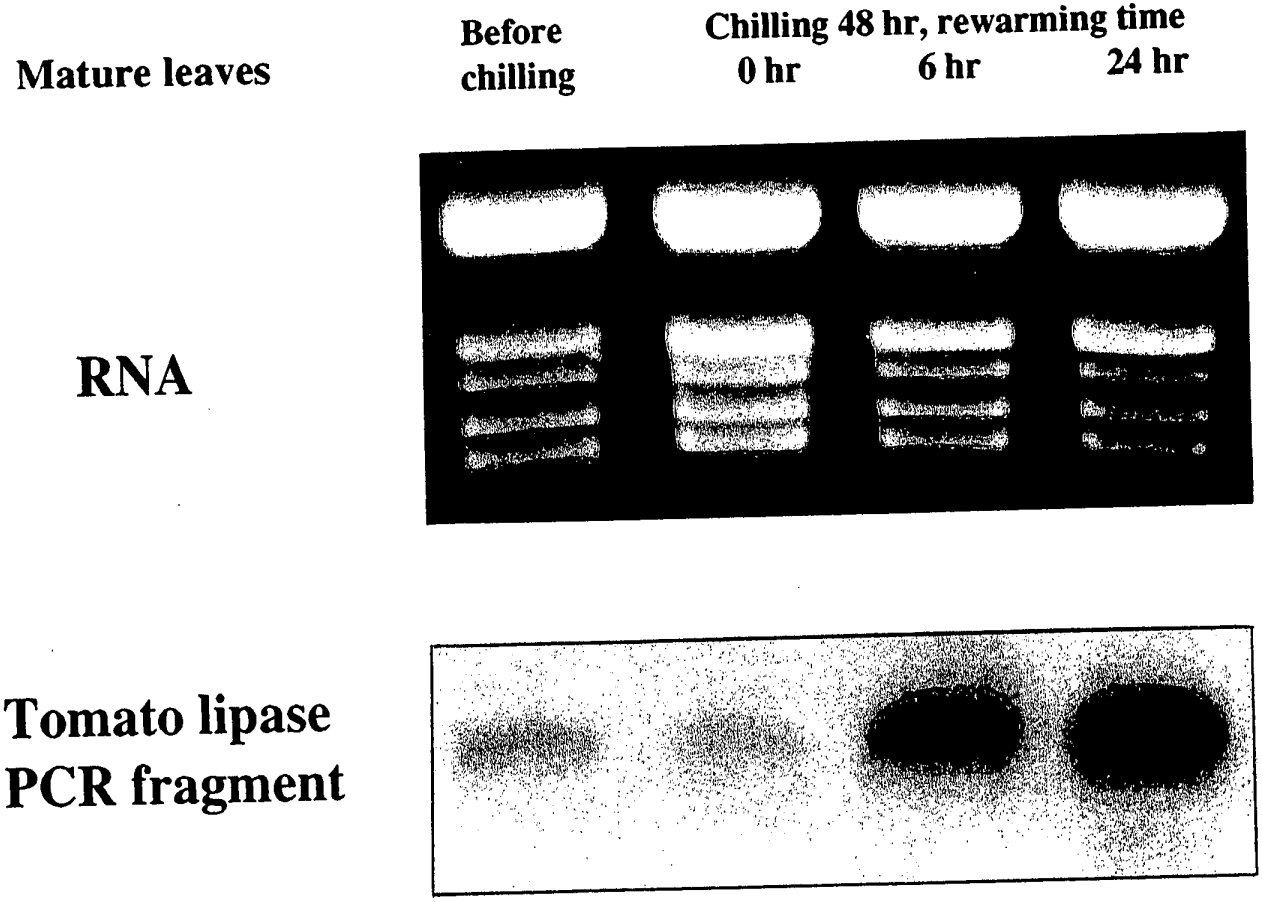


FIG.12

```
1/1                                                 31/11                                                61/21
CGG GTC GAC CCA CGC GTC CGC GAA AAC GCT TCC GAC TAC GAg GTT GTA AAC TTC CTC TAC GCC ACA GCT CGT GTT TCT CTC CCC GAA GGT
R   V   D   P   R   V   R   E   N   A   S   D   Y   E   V   V   N   F   L   Y   A   T   A   R   V   S   L   P   E   G
91/31                                               121/41                                               151/51
TTG CTT CTC CAA TCA CAA TCA AGA gAT TCT TGG GAC CGT GAG TCT AAC TGG TTT GGC TAC ATT GCT GTC ACG TCT GAT GAA CGG TCT AAG
L   L   L   Q   S   Q   S   R   D   S   W   D   R   E   S   N   W   F   G   Y   I   A   V   T   S   D   E   R   S   K
181/61                                              211/71                                               241/81
GCT TTA GGA CGC CGT GAG ATC TAT ATA GCT TTG AGA GGA ACG AGC AGG AAC TAT GAG TGG GTC AAT GTT TTG GGT GCT AGG CCA ACT TCA
A   L   G   R   R   E   I   Y   I   A   L   R   G   T   S   R   N   Y   E   W   V   N   V   L   G   A   R   P   T   S
271/91                                              301/101                                              331/111
GCT GAC CCC TTG CTG CAC GGA CCC GAG CAG GAT GGT TCT GGT GGT GTA GTT GAA GGT ACG ACT TTT GAT AGT GAC AGT GAA GAT GAA GAA
A   D   P   L   L   H   G   P   E   Q   D   G   S   G   G   V   V   E   G   T   T   F   D   S   D   S   E   D   E   E
361/121                                             391/131                                              421/141
GGG TGT AAG GTG ATG CTC GGG TGG CTC ACA ATC TAT ACT TCT AAT CAC CCC GAA TCG AAA TTC ACT AAG CTG AGT CTA CGG TCA CAG TTG
G   C   K   V   M   L   G   W   L   T   I   Y   T   S   N   H   P   E   S   K   F   T   K   L   S   L   R   S   Q   L
451/151                                             481/161                                              511/171
TTA GCC AAG ATC AAG GAG CTT CTG TTG AAG TAT AAG GAC GAG AAA CCG AGC ATT GTG TTG ACT GGA CAT AGC TTG GGA CCT ACA GAG GCT
L   A   K   I   K   E   L   L   L   K   Y   K   D   E   K   P   S   I   V   L   T   G   H   S   L   G   A   T   E   A
541/181                                             571/191                                              601/201
GTT CTG GCC GCC TAT GAT ATA GCT GAG AAC GGT TCC AGT GAT GAT GTT CCG GTC ACT GCT ATA GTC TTT GGT TGT CCA CAG GTA GGA AAC
V   L   A   A   Y   D   I   A   E   N   G   S   S   D   D   V   P   V   T   A   I   V   F   G   C   P   Q   V   G   N
631/211                                             661/221                                              691/231
AAG GAG TTC AGA GAC GAA GTA ATG AGT CAC AAG AAC TTA AAG ATC CTC CAT GTA AGG AAC ACG ATT GAT CTC TTA ACT CGA TAC CCA GGG
K   E   F   R   D   E   V   M   S   H   K   N   L   K   I   L   H   V   R   N   T   I   D   L   L   T   R   Y   P   G
```

FIG.13A

```
721/241                                    751/251                                    781/261
GGA CTT TTA GGG TAT GTG GAC ATA GGa ATA AAC TTT GTG ATC GAT ACA AAG AAG TCA CCG TTC CTA AGC GAT TCA AGG AAT CCA GGG GAT
G   L   L   G   Y   V   D   I   G   I   N   F   V   I   D   T   K   K   S   P   F   L   S   D   S   R   N   P   G   D
811/271                                    841/281                                    871/291
TGG CAT AAT cTT CAG GCG ATG TTA CAT GTT GTA GCT GGA TGG AAT GGG AAG AAA GGA GAG TTT AAA CTG ATG GTT AAG AGA AGT ATT GCA
W   H   N   L   Q   A   M   L   H   V   V   A   G   W   N   G   K   K   G   E   F   K   L   M   V   K   R   S   I   A
901/301                                    931/311                                    961/321
TTA GTG AAC AAG TCA TGC GAG TTc TTG AAA GCT GAG TGT TTG GTG CCA GGA TCT TGG TGG GTA GAG AAG AAC AAA GGA CTG ATC AAG AAC
L   V   N   K   S   C   E   F   L   K   A   E   C   L   V   P   G   S   W   W   V   E   K   N   K   G   L   I   K   N
991/331                                    1021/341                                   1051
GAA GAT GGT GAA TGG GTT cTT GCT CCC GTT GAA GAA GAA CCT GTA CCT GAA TTC TAA ATT GTA TTT CTG TAT TTT TCT CTA AGG TCA TGA
E   D   G   E   W   V   L   A   P   V   E   E   E   P   V   P   E   F   *
                                                                                      1141                                   1165
1081                                       1111
TAA ATC AAC AAT AAG CAG TTC AAC TAT GTG ATG AAA AGA CCC AAG TTA TTA TAT TGA TAT GAG TTT ATG AGA TAA AAA AAA AAA AAA
```

Note: The identity of nucleotides indicated in lower case needs to be confirmed.

FIG.13B

Sequence of *Aradopsis thaliana* senescence lipase

```
ATGACGGCGGAAGATATTCGCCGGCGAGATAAAAAAACCGAAGAAGAAAGAAGACTAAGAG
 M  T  A  E  D  I  R  R  R  D  K  K  T  E  E  E  R  R  L  R
ACACGTGGCGTAAGATCCAAGGAGAAGACGATTGGGCCGGGTTAATGGATCCAATGGATCCA
 D  T  W  R  K  I  Q  G  E  D  D  W  A  G  L  M  D  P  M  D  P
ATTCTTAGATCGGAGCTAATCCGTTACGGCGAAATGGCTCAAGCTTGTTACGACGCTTTCGAT
 I  L  R  S  E  L  I  R  Y  G  E  M  A  Q  A  C  Y  D  A  F  D
TTCGATCCCGCTTCCAAATACTGCGGCACCTCCAGGTTCACGCGACTCGAGTTCTTCGATTCTC
 F  D  P  A  S  K  Y  C  G  T  S  R  F  T  R  L  E  F  F  D  S
TCGGAATGATCGATTCCGGTTACGAGGTGGCGCGTTACCTCTACGCGACGTCGAACATCAATC
 L  G  M  I  D  S  G  Y  E  V  A  R  Y  L  Y  A  T  S  N  I  N
TCCCGAACTTCTTCTCGAAATCGCGGTGGTCTAAAGTCTGGAGCAAAAACGCTAATTGGATGG
 L  P  N  F  F  S  K  S  R  W  S  K  V  W  S  K  N  A  N  W  M
GATACGTCGCCGTTTCAGACGACGAAACGTCTCGTAACCGACTCGGCCGCCGTGATATCGCGA
 G  Y  V  A  V  S  D  D  E  T  S  R  N  R  L  G  R  R  D  I  A
TTGCGTGGAGAGGAACCGTTACGAAACTTGAATGGATCGCGGATCTAAAGGATTATTTAAAA
 I  A  W  R  G  T  V  T  K  L  E  W  I  A  D  L  K  D  Y  L  K
CCGGTAACCGAAAACAAGATCCGATGCCCCGACCCGGCCGTTAAAGTCGAATCCGGATTCTTA
 P  V  T  E  N  K  I  R  C  P  D  P  A  V  K  V  E  S  G  F  L
GATCTCTACACTGACAAAGACACAACCTGCAAATTCGCGAGATTCTCAGCGCGTGAACAGATT
 D  L  Y  T  D  K  D  T  T  C  K  F  A  R  F  S  A  R  E  Q  I
TTAACGGAGGTGAAACGGTTAGTGGAAGAACACGGCGACGACGATGATTCCGATTTAAGCAT
 L  T  E  V  K  R  L  V  E  E  H  G  D  D  D  D  S  D  L  S  ■
CACCGTGACGGGACACAGTCTCGGCGGCGCGTTAGCGATATTAAGCGCGTACGATATAGCGG
 [redacted]  A  L  A  I  L  S  A  Y  D  I  A
AGATGAGATTGAATCGGAGTAAGAAAGGGAAAGTGATTCCGGTGACGGTGTTGACATACGGA
 E  M  R  L  N  R  S  K  K  G  K  V  I  P  V  T  V  L  T  Y  G
GGACCGAGAGTTGGGAACGTTAGGTTTAGGGAGAGGATGGAGGAATTGGGAGTGAAAGTGAT
 G  P  R  V  G  N  V  R  F  R  E  R  M  E  E  L  G  V  K  V  M
GAGAGTAGTGAATGTTCACGACGTGGTTCCCAAGTCGCCGGGATTGTTTTTGAACGAGAGTAG
 R  V  V  N  V  H  D  V  V  P  K  S  P  G  L  F  L  N  E  S  R
ACCTCACGCGCTGATGAAGATAGCGGAGGGGTTGCCGTGGTGTTATAGCCACGTGGGGGAGG
 P  H  A  L  M  K  I  A  E  G  L  P  W  C  Y  S  H  V  G  E
AGCTGGCGTTGGATCATCAGAACTCGCCGTTTCTTAAACCTTCCGTTGATGTTTCTACTGCTCA
E  L  A  L  D  H  Q  N  S  P  F  L  K  P  S  V  D  V  S  T  A  H
TAATCTTGAAGCTATGCTTCATTTACTTGACGGGTATCATGGAAAAGGAGAGAGATTTGTGCT
 N  L  E  A  M  L  H  L  L  D  G  Y  H  G  K  G  E  R  F  V  L
GTCGAGTGGGAGAGACCATGCGCTAGTGAACAAAGCGTCGGACTTTTTGAAAGAGCATTTAC
 S  S  G  R  D  H  A  L  V  N  K  A  S  D  F  L  K  E  H  L
AAATTCCACCGTTTTGGCGTCAAGACGCGAATAAAGGAATGGTTCGGAACAGTGAAGGTCGT
Q  I  P  P  F  W  R  Q  D  A  N  K  G  M  V  R  N  S  E  G  R
TGGATTCAAGCCGAGCGTCTCCGTTTTGAGGATCATCATTCTCCTGATATCCACCACCATCTCT
 W  I  Q  A  E  R  L  R  F  E  D  H  H  S  P  D  I  H  H  H  L
CTCAGCTCCGTCTTGATCATCCTTGTTAA
S  Q  L  R  L  D  H  P  C
```

FIG.14

Northern Blot of Aging *Arabidopsis thaliana* Leaf Tissue

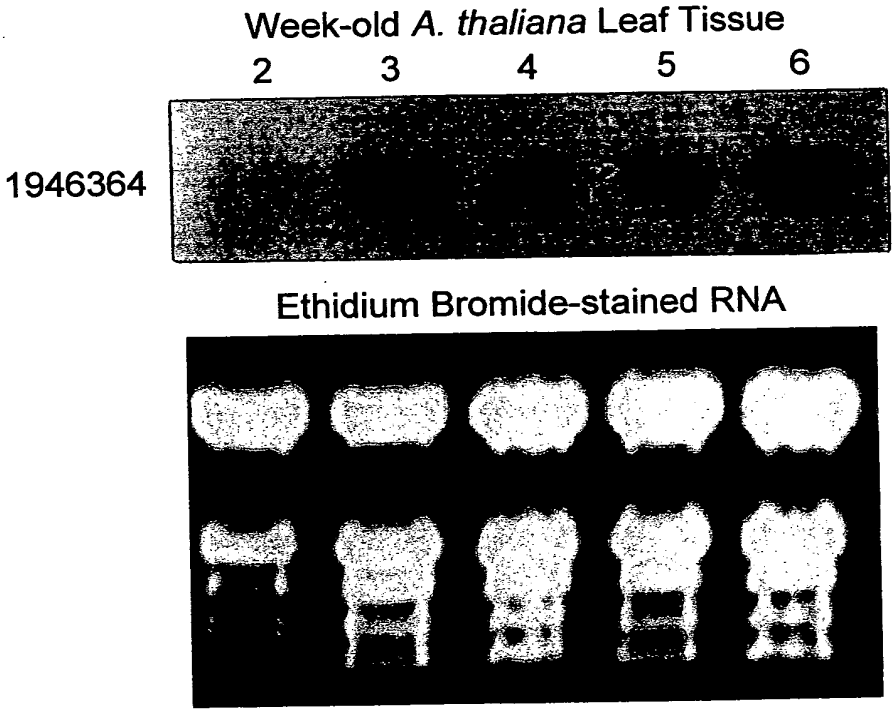


FIG.15

Northern Blot of Ethephon-treated
Arabidopsis thaliana Leaf Tissue

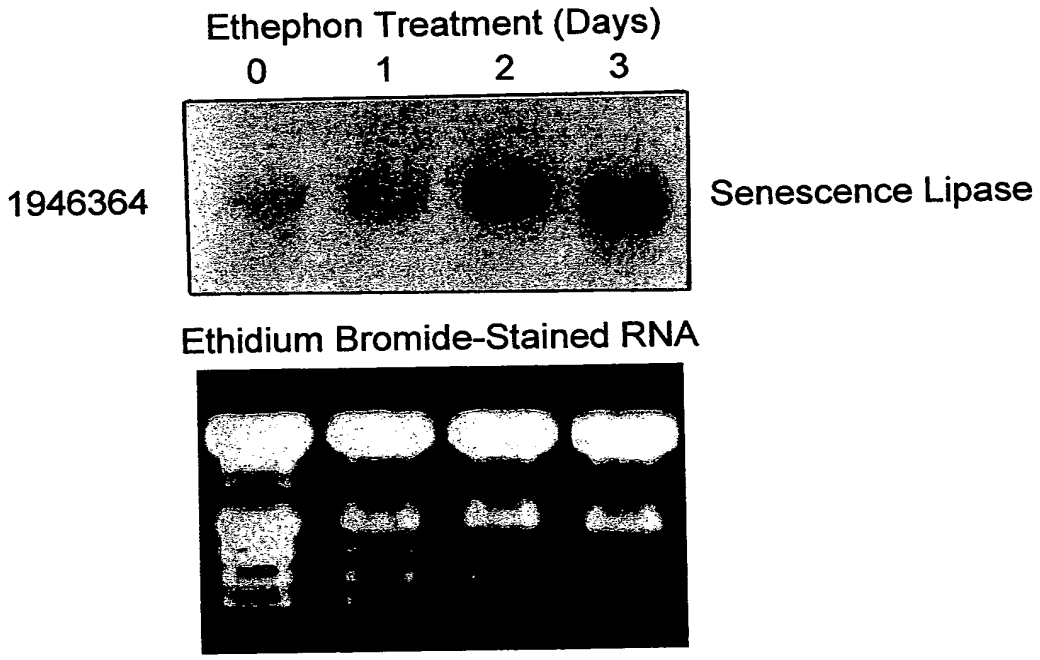


FIG.16

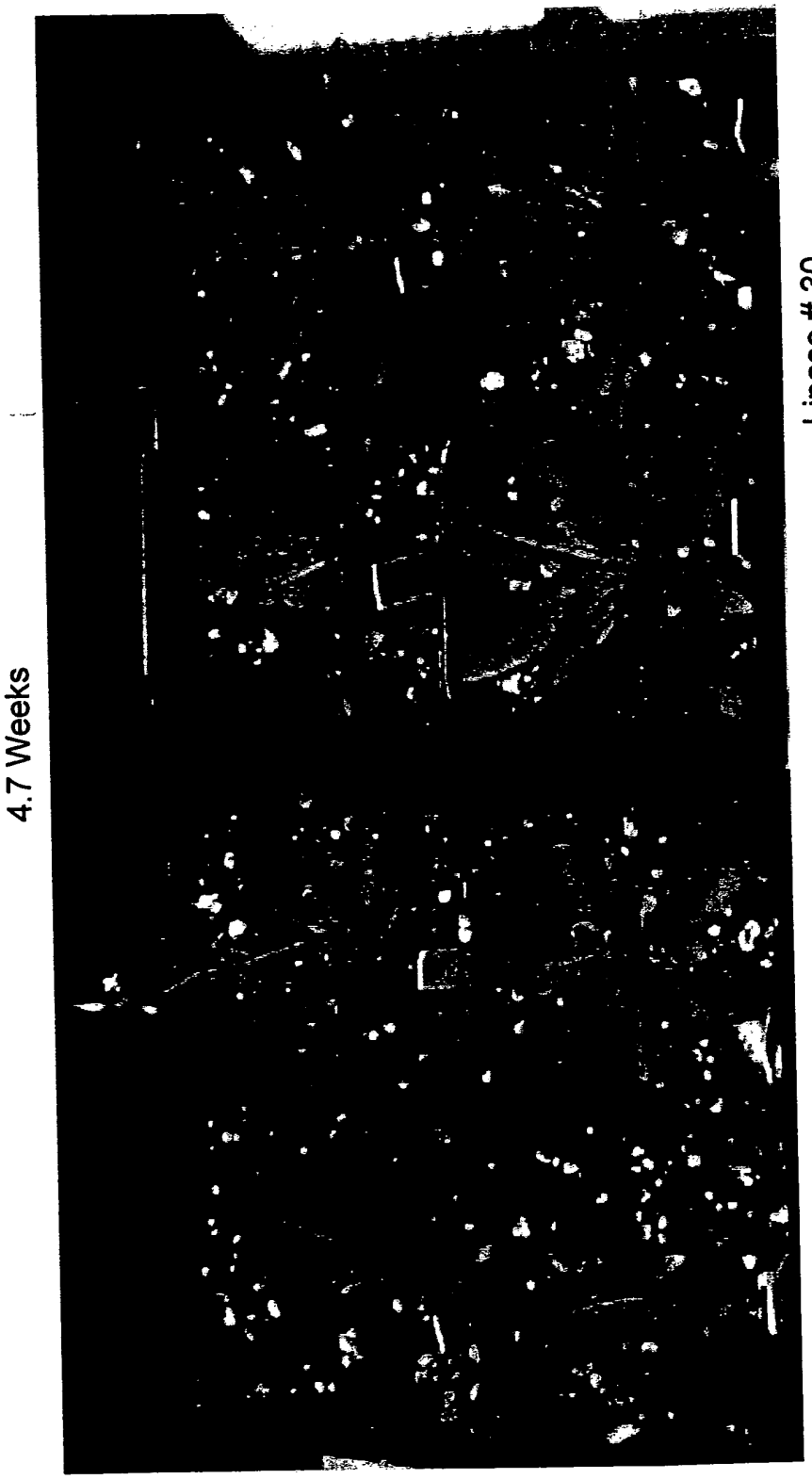
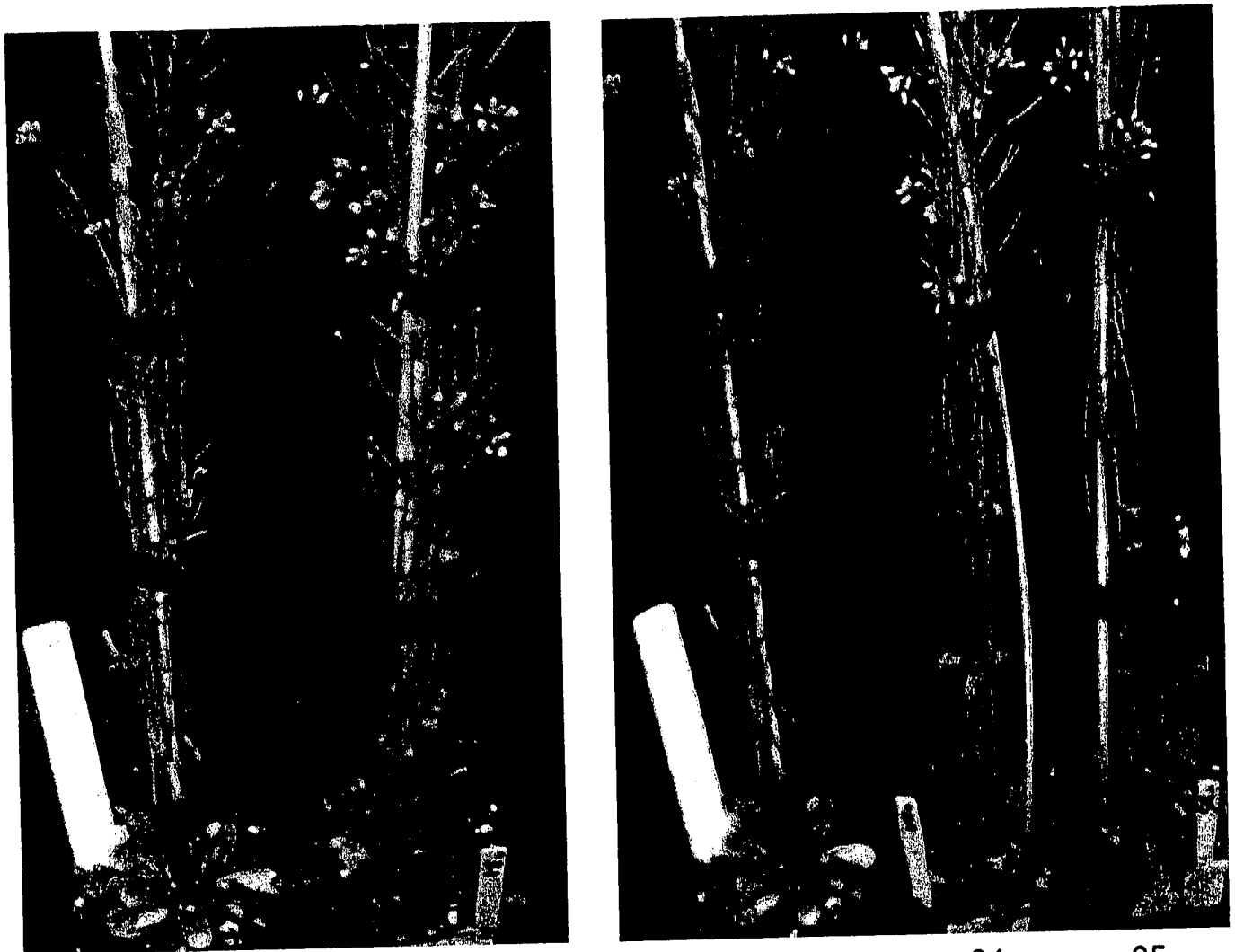


FIG.17

6.3 Weeks



WT 31 WT 34 35

FIG.18

7 Weeks

Wild-Type α -Lipase # 9

FIG.19

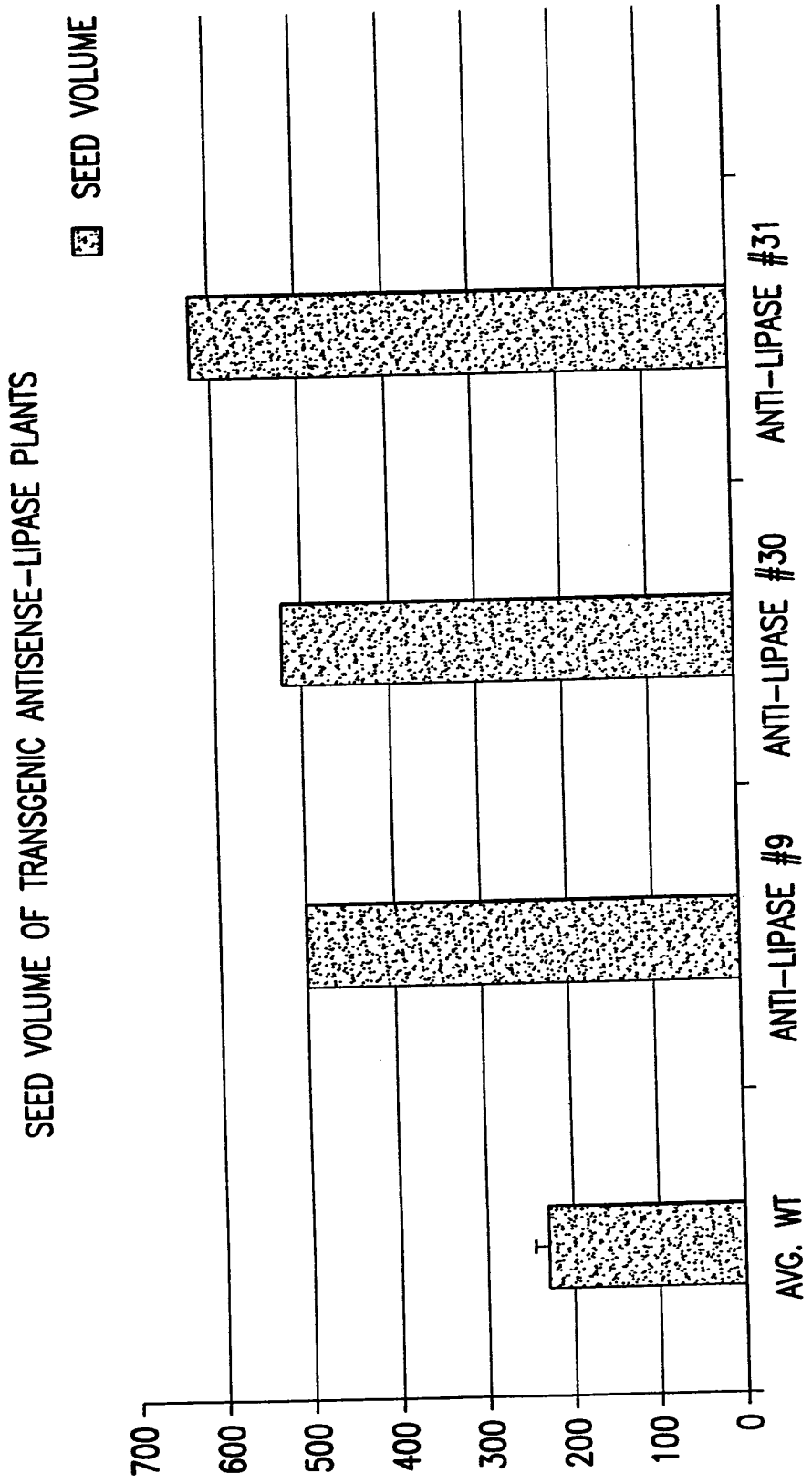

SEED VOLUME OF TRANSGENIC ANTISENSE-LIPASE PLANTS
SEED VOLUME
700
600
500
400
300
200
100
0
AVG. WT
ANTI-LIPASE #9
ANTI-LIPASE #30
ANTI-LIPASE #31
PLANT LINE

FIG. 20

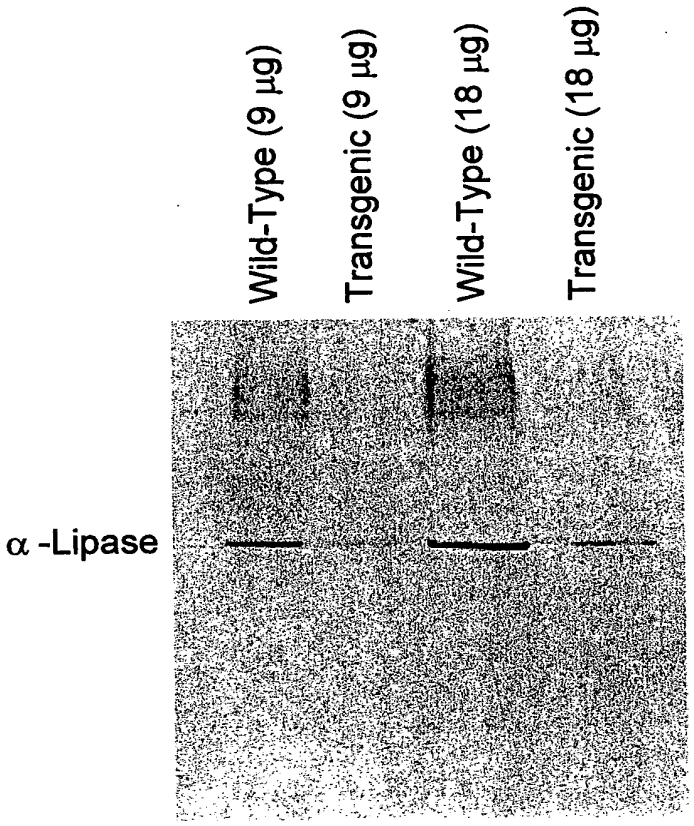


FIG.21